

Db 1861 GCACGAGAGTCAAGTGGGGGCTGGACCAAGAGCGGAGGCCCGGCTGACCG 1920  
 QY 639 YSERIALALALEUGINPROLEUENHISHTHVALVSAAGLYSERPROSERASPMECTR 659  
 Db 1921 TAGCCCGCCCTGCAACCCCTCTGTGACACGGGAAAGCGGACGCCCTCTGACATGCC 1980  
 QY 659 CARGASERGIYILETYRASPSESERVALPROSESERGIULEUSETLEUENHISHTH 679  
 Db 1981 GGGGACCTCAGCACTTATGACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
 QY 679 TGLUIGLYSESRTHRASPGLNTHRLINHTSERSETHRGLUSERVALSERSE 699  
 Db 2041 GGAAGACCTCTGACGACCAAGAAAGCTTCCCTGACGAGAGGCTGCTCC 2100  
 QY 699 TSEGLYLEUGLYGLUGLUPROFALALEUPROSERLYLEUENHISHTH 719  
 Db 2101 TTCAGGCTGCTGAGGAGAACCTTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
 QY 719 TCYALVALAASPGLNGLYCVALISERTHTHASPGLNGLUENHISHTHVALAVALA 738  
 Db 2161 ATGCAAGACAGATCTTGTTGCGGAGCTACAGTGAATCCACGCGGTGCGCCCT 2218

RESULT 14  
 US-09-863-818A-9  
 Sequence 9, Application US/09863818A  
 Publication No. US20030092881A1  
 GENERAL INFORMATION:  
 APPLICANT: Gorman, Daniel M.  
 TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS  
 FILE REFERENCE: DX01170K  
 CURRENT APPLICATION NUMBER: US/09/863,818A  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/206,862  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 9  
 LENGTH: 2786  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURES:  
 NAME/KEY: CDS  
 LOCATION: (70)..(2283)  
 OTHER INFORMATION:  
 NAME/KEY: mat\_peptide  
 LOCATION: (118)..()  
 OTHER INFORMATION:  
 NAME/KEY: misc\_feature  
 LOCATION: (8)..(8)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (144)..(144)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (170)..(170)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (194)..(194)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (442)..(442)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (475)..(475)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (519)..(519)  
 OTHER INFORMATION: unknown amino  
 US-09-863-818A-9

Alignment Scores: 0 Length: 2786  
 Pred. No.: 0

Score: 3835.50 Matches: 722  
 Percent Similarity: 98.24 Conservative: 3  
 Best Local Similarity: 97.84 Mismatches: 12  
 Query Match: 97.24 Indels: 1  
 DB: 3 Gaps: 1

US-10-616-788-2 (1-738) x US-09-863-818A-9 (1-2786)

QY 1 METALAPROTHLEUGINLEUCYSESERVALPHEPETHVALAVALAVALAVALAVALA 20  
 Db 70 ATGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129  
 QY 21 SERGILEUVALAVALAVALAVALAVALAVALAVALAVALAVALAVALAVALAVALA 40  
 Db 130 TGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 189  
 QY 41 TPARGLYVALAVALAVALAVALAVALAVALAVALAVALAVALAVALAVALAVALA 60  
 Db 190 TGGANGGAGTGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 249  
 QY 61 ASPHENVYTHRTHTYRLEUASNPVOVALGLYLSHISVALLEALASPALAGLASN 80  
 Db 250 GACAAATGTACCACTTACTTGAATCAAGTGGGAAAGCAATGATGCTGACGCGCCAGAT 309  
 QY 81 ILETHRLIESERGINYRVALAVALAVALAVALAVALAVALAVALAVALAVALAVALA 100  
 Db 310 ATCAACATCAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369  
 QY 101 GLVALALEUGLYILEGLUPHELEUENHISHTHVALVSAAGLYSERPROSERASPMECTR 120  
 Db 370 GGGGCGCTCGGCACTGCAATCTCTGAAGGATTTGGGTAATACAGGAGAGCTGAGTGC 429  
 QY 121 GLUGLYARGGLNGLYGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 140  
 Db 430 GAGGGAAGACAGAGCCCAACCACTATTTCAAGATCCGAGAGCAAGNTCAACAGTAGCTTC 489  
 QY 141 LYSARGHRTHTHTYRLEUASNPVOVALGLYLSHISVALLEALASPALAGLASN 160  
 Db 490 AAAGAACTGGAATGAAATCTCACTTCTGAAATGAAATGAAATGAAATGAAATGAAATGAA 549  
 QY 161 VALYVALAVALAVALAVALAVALAVALAVALAVALAVALAVALAVALAVALAVALA 180  
 Db 550 GTAAG---TTGCTCTTCT 606  
 QY 181 ARGTHRARGALACYSAPLEULEUENHISHTHVALVSAAGLYSERPROSERASPMECTR 200  
 Db 607 AGAACCCGAGCTGTGACTGTGTGTGACGCGGACCAATCTGATTAACCTTCTGCG 666  
 QY 201 LYSARGHRTHTHTYRLEUASNPVOVALGLYLSHISVALLEALASPALAGLASN 220  
 Db 667 AAGCTTCGGAACCTGAACTCAAGCAGATGCTGCAATGAGTGTCTTCTGACAC 726  
 QY 221 ALAPROTHLEUGINLEUCYSESERVALPHEPETHVALAVALAVALAVALAVALAVALA 240  
 Db 727 GCACCGCAACACTTCCGCTTCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 786  
 QY 241 PROPHELYARGLYSRHTYRGLYGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 260  
 Db 787 CTTTCAAGGAAAGACTGTAAGCAGAGCAACCTACAGAGATGACAGCTGCTCTCT 846  
 QY 261 GLHASNVALSERPROGLYASPTYRILEGLILEUVALASPAPHTHRTHTHRTHTHRT 280  
 Db 847 CAANAATGTTCTCCAGGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 906  
 QY 281 LYSVALMECHISTYRVALALEUVALPVOVALHISERPROTPALAGLYPROTILARALA 300  
 Db 907 AAAGTGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 966  
 QY 301 METALALEUVALPROLEUENHISHTHVALVSAAGLYSERPROSERASPMECTR 320  
 Db 967 GTGGCATCAAGTGGCACTGTGATCTATTCGCAATTCGCAATTCGCAATTCGCAATTCG 1026  
 QY 321 CYARGLYSLYGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 340

D	b		2107	GGA	CTCCAGCGGACCA	CAGACAGAAACGTTCCTGCCTGACGAGAAGGTGGTCTCTTCA	2166
O	y		701	GLY	LEUGLIGLU	GIUPLUPPOALALEUPROSERIVLEULENSERSERLYSERYCYS	720
D	b		2167	GG	CTGGTGGA	GGAGGAACTCTGCTTCCTTCCTTCACACTCTCTCTTTGGTATGC	2226
O	y		721	LVEA	LAAPLEULIYCYSAR	SERTYTRHRAAGJULUEHLALAVALAPro	738
D	b		2227	AANG	CAATCTTGITGCCG	AGCTACACTGATGAATCCAAGCGTGGCCCCCT	2280
 RESULT 15 US-10-749-144-9							
; Sequence 9, Application US/10749144							
Publication No. US20040197306A1							
GENERAL INFORMATION:							
APPLICANT: Gorman, Daniel M.							
TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS							
FILE REFERENCE: DX011701							
CURRENT APPLICATION NUMBER: US/10/749,144							
CURRENT FILING DATE: 2003-12-29							
PRIOR APPLICATION NUMBER: US 60/206,862							
PRIOR FILING DATE: 2000-05-24							
NUMBER OF SEQ ID NOS: 24							
SOFTWARE: PatentIn version 3.2							
SEQ ID NO 9							
LENGTH: 2786							
TYPE: DNA							
ORGANISM: Homo sapiens							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (8)..(8)							
OTHER INFORMATION: unknown amino							
FEATURE:							
NAME/KEY: CDS							
LOCATION: (70)..(2283)							
FEATURE:							
NAME/KEY: mat_peptide							
LOCATION: (118)..()							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (144)..(144)							
OTHER INFORMATION: unknown amino							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (170)..(170)							
OTHER INFORMATION: unknown amino							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (194)..(194)							
OTHER INFORMATION: unknown amino							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (442)..(442)							
OTHER INFORMATION: unknown amino							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (475)..(475)							
OTHER INFORMATION: unknown amino							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: (519)..(519)							
OTHER INFORMATION: unknown amino							
US-10-749-144-9							
 Alignment Scores:							
Pred. No.:           0							
Percent Similarity: 3835.50							
Best Local Similarity: 98.2%							
Query Match: 97.8%							
DB: 8							
Length: 2786							
Matches: 722							
Conservative: 3							
Mismatches: 12							
Indels: 1							
Gaps: 1							

QY 587 VLVNWKPPESPDPCLKVEAPVLGATGAPADSOHESOHGGLDGEARPALDGSAAIPL 646  
 DB 601 VLVNWKPPESPDPCLKVEAPVLGATGAPADSOHESOHGGLDGEARPALDGSAAIPL 660  
 QY 647 LHTVAKGSPDMPDPSGIDYSSVPSSELSLPLMEGLSTDQETISLTESVSSSGLGEE 706  
 DB 661 LHTVAKGSPDMPDPSGIDYSSVPSSELSLPLMEGLSTDQETISLTESVSSSGLGEE 720  
 QY 707 PPALPSTLSSGCKADLGRSTYDELHAAVP 738  
 DB 721 PPALPSTLSSGCKADLGRSTYDELHAAVP 752

RESULT 13

US-09-863-818A-10  
 Sequence 10, Application US/09863818A  
 Publication No. US20030092881A1  
 GENERAL INFORMATION:  
 APPLICANT: Gorman, Daniel M.  
 TITLE OR INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS  
 FILE REFERENCE: DX01170K  
 CURRENT APPLICATION NUMBER: US/09/863, 818A  
 PRIOR FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/206, 862  
 PRIOR FILING DATE: 2000-05-24  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 10  
 LENGTH: 738  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (18)..(18)  
 OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.  
 NAME/KEY: misc\_feature  
 LOCATION: (26)..(26)  
 OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.  
 NAME/KEY: misc\_feature  
 LOCATION: (109)..(109)  
 OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.  
 NAME/KEY: misc\_feature  
 LOCATION: (120)..(120)  
 OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.  
 NAME/KEY: misc\_feature  
 LOCATION: (134)..(134)  
 OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.  
 NAME/KEY: misc\_feature  
 LOCATION: (8)..(8)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (144)..(144)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (194)..(194)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (442)..(442)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (475)..(475)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc\_feature  
 LOCATION: (519)..(519)  
 OTHER INFORMATION: unknown amino  
 US-09-863-818A-10

Query Match 97.2%; Score 1835.5; DB 3; Length 738;  
 Best Local Similarity 97.8%; Pred. No. 0;

Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 MAPMLQCSVFETVNAKCLNGSOLAIVAAGSGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60  
 DB 1 MAPMLQCSVFETVNAKCLNGSOLAIVAAGSGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60  
 QY 61 DNTCTYLANPVKGVIAADQNTTISOYACHDOVAVTLLMSFGALGIBPLKGRVILELKS 120  
 DB 61 DNTCTYLANPVKGVIAADQNTTISOYACHDOVAVTLLMSFGALGIBPLKGRVILELKS 120  
 QY 121 EGRQCCOQLIKDPOKLNSSFKRTGMSOPFLNKKFTDYVKKVPPSTONENYHFFP 180  
 DB 121 EGRQCCOQLIKDPOKLNSSFKRTGMSOPFLNKKFTDYVKKVPPSTONENYHFFP 180  
 QY 181 RTACDLILQPDMLACKPFWKPRNLNISOHSDMOVSFDHAPNFGFRFYLYHKLKHEG 240  
 DB 181 RTACDLILQPDMLACKPFWKPRNLNISOHSDMOVSFDHAPNFGFRFYLYHKLKHEG 240  
 QY 241 PFRKTKCKOETETTSCLLQNVSPGDYIIEVVDNTTRKVMHYALKPVHSPWAGIRA 300  
 DB 241 PFRKTKCKOETETTSCLLQNVSPGDYIIEVVDNTTRKVMHYALKPVHSPWAGIRA 300  
 QY 301 MALTPLVVISAPATLFTWCKRKKOENIYSHDESSSSTTALPRRLAPRRVFL 360  
 DB 301 MALTPLVVISAPATLFTWCKRKKOENIYSHDESSSSTTALPRRLAPRRVFL 360  
 QY 361 CYSSKOGONMNVVQCFAYFLDPCGCEVALDMEDPSLCREGRKENVIOKHESQFIIV 420  
 DB 361 CYSSKOGONMNVVQCFAYFLDPCGCEVALDMEDPSLCREGRKENVIOKHESQFIIV 420  
 QY 421 VCSKGMKTFVDKKNYKHKGGSGKGLFLVAVSAIAEKLRQAKOSSAALSKFLAVYF 480  
 DB 421 VCSKGMKTFVDKKNYKHKGGSGKGLFLVAVSAIAEKLRQAKOSSAALSKFLAVYF 480  
 QY 481 DYSCEGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGHTQGSRRNTFRSSGR 540  
 DB 481 DYSCEGDVPGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGHTQGSRRNTFRSSGR 540  
 QY 541 SLTVAILCNMHOPIDEBPDMERKOFVPHPPPLRYRBPVLEKPSGLVLDVWCKPPESP 600  
 DB 541 SLTVAILCNMHOPIDEBPDMERKOFVPHPPPLRYRBPVLEKPSGLVLDVWCKPPESP 600  
 QY 601 FCLKVEAPVLGATGAPADSOHESOHGGLDGEARPALDGSAAIPLHTVAKGSPDMPR 660  
 DB 601 FCLKVEAPVLGATGAPADSOHESOHGGLDGEARPALDGSAAIPLHTVAKGSPDMPR 660  
 QY 660 DSGIYDSSVPSSELSLPLMEGLSTDQETISLTESVSSSGLGEEPPALPSTLSSGSC 720  
 DB 660 DSGIYDSSVPSSELSLPLMEGLSTDQETISLTESVSSSGLGEEPPALPSTLSSGSC 720  
 QY 721 KADLGRSTYDELHAAVP 738  
 DB 721 KADLGRSTYDELHAAVP 738

RESULT 14

US-10-749-144-10  
 Sequence 10, Application US/10749144  
 Publication No. US20040197306A1  
 GENERAL INFORMATION:  
 APPLICANT: Gorman, Daniel M.  
 TITLE OR INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS  
 FILE REFERENCE: DX01170K1  
 CURRENT APPLICATION NUMBER: US/10/749, 144  
 PRIOR FILING DATE: 2003-12-29  
 PRIOR APPLICATION NUMBER: US 60/206, 862  
 PRIOR FILING DATE: 2000-05-24  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 10  
 LENGTH: 738  
 TYPE: PRT  
 ORGANISM: Homo sapiens